



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/051,644C

DATE: 10/01/2004

TIME: 11:08:15

Input Set : A:\Cam-0121.app

Output Set: N:\CRF4\10012004\J051644C.raw

3 <110> APPLICANT: Liu, et al.
 5 <120> TITLE OF INVENTION: Screens and Assays for Agents Useful in Controlling
 6 Parasitic Nematodes
 8 <130> FILE REFERENCE: 2002630-0012
 10 <140> CURRENT APPLICATION NUMBER: 10/051,644C
 11 <141> CURRENT FILING DATE: 2002-01-18
 13 <160> NUMBER OF SEQ ID NOS: 8
 15 <170> SOFTWARE: PatentIn Ver. 2.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 425
 19 <212> TYPE: PRT
 20 <213> ORGANISM: Artificial Sequence
 22 <220> FEATURE:
 23 <223> OTHER INFORMATION: Description of Artificial Sequence:VAP-1 Amino
 24 Acid Sequence
 26 <400> SEQUENCE: 1
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 28 1 5 10 15
 30 Val Ala Gln Thr Phe Gly Cys Ser Asn Thr Lys Ile Asn Asp Gln Ala
 31 20 25 30
 33 Arg Lys Met Phe Tyr Asp Ala His Asn Asp Ala Arg Arg Ser Met Ala
 34 35 40 45
 36 Lys Gly Leu Glu Pro Asn Lys Cys Gly Leu Leu Ser Gly Gly Lys Asn
 37 50 55 60
 39 Val Tyr Glu Leu Asn Trp Asp Cys Glu Met Glu Ala Lys Ala Gln Glu
 40 65 70 75 80
 42 Trp Ala Asp Gly Cys Pro Ser Ser Phe Gln Thr Phe Asp Pro Thr Trp
 43 85 90 95
 45 Gly Gln Asn Tyr Ala Thr Tyr Met Gly Ser Ile Ala Asp Pro Leu Pro
 46 100 105 110
 48 Tyr Ala Ser Met Ala Val Asn Gly Trp Trp Ser Glu Ile Arg Thr Val
 49 115 120 125
 51 Gly Leu Thr Asp Pro Asp Asn Lys Tyr Thr Asn Ser Ala Met Phe Arg
 52 130 135 140
 54 Phe Ala Asn Met Ala Asn Gly Lys Ala Ser Ala Phe Gly Cys Ala Tyr
 55 145 150 155 160
 57 Ala Leu Cys Ala Gly Lys Leu Ser Ile Asn Cys Ile Tyr Asn Lys Ile
 58 165 170 175
 60 Gly Tyr Met Thr Asn Ala Ile Ile Tyr Glu Lys Gly Asp Ala Cys Thr
 61 180 185 190
 63 Ser Asp Ala Glu Cys Thr Thr Tyr Ser Asp Ser Gln Cys Lys Asn Gly
 64 195 200 205
 66 Leu Cys Tyr Lys Ala Pro Gln Ala Pro Val Val Glu Thr Phe Thr Met

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69 Cys Pro Ser Val Thr Asp Gln Ser Asp Gln Ala Arg Gln Asn Phe Leu
70 225      230      235      240
72 Asp Thr His Asn Lys Leu Arg Thr Ser Leu Ala Lys Gly Leu Glu Ala
73      245      250      255
75 Asp Gly Ile Ala Ala Gly Ala Phe Ala Pro Met Ala Lys Gln Met Pro
76      260      265      270
78 Lys Leu Val Lys Tyr Ser Cys Thr Val Glu Ala Asn Ala Arg Thr Trp
79      275      280      285
81 Ala Lys Gly Cys Leu Tyr Gln His Ser Thr Ser Ala Gln Arg Pro Gly
82      290      295      300
84 Leu Gly Glu Asn Leu Tyr Met Ile Ser Ile Asn Asn Met Pro Lys Ile
85 305      310      315      320
87 Gln Thr Ala Glu Asp Ser Ser Lys Ala Trp Trp Ser Glu Leu Lys Asp
88      325      330      335
90 Phe Gly Val Gly Ser Asp Asn Ile Leu Thr Gln Ala Val Phe Asp Arg
91      340      345      350
93 Gly Val Gly His Tyr Thr Gln Met Ala Trp Glu Gly Thr Thr Glu Ile
94      355      360      365
96 Gly Cys Phe Val Glu Asn Cys Pro Thr Phe Thr Tyr Ser Val Cys Gln
97      370      375      380
99 Tyr Gly Pro Ala Gly Asn Tyr Met Asn Gln Leu Ile Tyr Thr Lys Gly
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121 aatgatgcaa gacgaagcat ggctaaaggg cttgagccaa acaagtgcgg actcttatct 180
122 ggtggaaaga atgtttatga attgaattgg gattgcgaga tggaagcaaa agctcaggaa 240
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124 gcgacgtaca tgggatcgat tgctgatccg cttccatacg cttccatggc tgttaattgg 360
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126 gcaatgttcc gatttgctaa tatggcaaat ggtaaagctt cagcttttgg atgtgcatac 480
127 gcgttggtcg caggaaaact atccatcaat tgcatttaca acaagatagg atacatgacc 540
128 aatgctatca tttatgaaaa aggagatgcc tgtaccagtg acgctgaatg caccacctac 600
129 tcagactcac aatgcaaaaa cggctcttgc tataaggcac ctcaagctcc agtcgttgag 660
130 actttcacia tgtgcccttc ggtcacggac cagtcggatc aggcgcgtca aaacttcttg 720
131 gacacccata acaaattgcg tacaagcctt gccaaaggac ttgaagctga tggaattgcc 780
132 gctggagcat ttgcaccaat ggccaagcaa atgccaaaac tggtaaaata cagctgcaca 840

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133 gttgaagcaa acgccagaac atgggcaaaa ggatgccttt accagcattc aacaagcgca 900
134 cagagaccag gactcgggtga aaatctttat atgatcagca ttaacaacat gcctaaaatt 960
135 caaaccgagg aggactctc aaaggcttgg tgggtccgagt tgaaagactt cggagtcggg 1020
136 tctgacaaca ttctgaccca agcagttttt gatcgtggcg ttggacatta cacacaaatg 1080
137 gcatgggaag gaactactga aattggatgt tttgtggaga attgtccaac attcacttat 1140
138 tccgtatgcc aatatgggtcc agcgggaaac tacatgaacc aactaatcta taccaagggc 1200
139 tcaccatgca cagctgacgc cgattgcccc ggaaccaga catgcagtgt cgctgaagca 1260
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160 Glu Gln Asn Val Trp Asn Asp Val Asp Asp Lys Val Val Glu Ala Leu
161           35           40           45
163 Gly Gly Leu Asp Asp Glu Leu Leu Thr Glu His Val Cys Asn Lys Ser
164           50           55           60
166 Thr Ile Thr Gln Leu Gln Gln Glu Ile Ile Leu Thr Thr His Asn Glu
167   65           70           75           80
169 Leu Arg Arg Ser Leu Ala Phe Gly Lys Gln Arg Asn Lys Arg Gly Leu
170           85           90           95
172 Met Asn Gly Ala Arg Asn Met Tyr Lys Leu Asp Trp Asp Cys Glu Leu
173           100          105          110
175 Ala Ser Leu Ala Ala Asn Trp Ser Thr Ser Cys Pro Gln His Phe Met
176           115          120          125
178 Pro Gln Ser Val Leu Gly Ser Asn Ala Gln Leu Phe Lys Arg Phe Tyr
179           130          135          140
181 Phe Tyr Phe Asp Gly His Asp Ser Thr Val His Met Arg Asn Ala Met
182 145          150          155          160
184 Lys Tyr Trp Trp Gln Gln Gly Glu Glu Lys Gly Asn Glu Asp Gln Lys
185           165          170          175
187 Asn Arg Phe Tyr Ala Arg Arg Asn Tyr Phe Gly Trp Ala Asn Met Ala
188           180          185          190
190 Lys Gly Lys Thr Tyr Arg Val Gly Cys Ser Tyr Ile Met Cys Gly Asp
191           195          200          205
193 Gly Glu Ser Ala Leu Phe Thr Cys Leu Tyr Asn Glu Lys Ala Gln Cys
194           210          215          220
196 Glu Lys Glu Met Ile Tyr Glu Asn Gly Lys Pro Cys Cys Glu Asp Lys
197 225          230          235          240
199 Asp Cys Phe Thr Tyr Pro Gly Ser Lys Cys Leu Val Pro Glu Gly Leu
200           245          250          255

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202 Cys Gln Ala Pro Ser Met Val Lys Asp Asp Gly Gly Ser Phe Gln Cys
203           260           265           270
205 Asp Asn Ser Leu Val Ser Asp Val Thr Arg Asn Phe Thr Leu Glu Gln
206           275           280           285
208 His Asn Phe Tyr Arg Ser Arg Leu Ala Lys Gly Phe Glu Trp Asn Gly
209           290           295           300
211 Glu Thr Asn Thr Ser Gln Pro Lys Ala Ser Gln Met Ile Lys Met Glu
212 305           310           315           320
214 Tyr Asp Cys Met Leu Glu Arg Phe Ala Gln Asn Trp Ala Asn Asn Cys
215           325           330           335
217 Val Phe Ala His Ser Ala His Tyr Glu Arg Pro Asn Gln Gly Gln Asn
218           340           345           350
220 Leu Tyr Met Ser Ser Phe Ser Asn Pro Asp Pro Arg Ser Leu Ile His
221           355           360           365
223 Thr Ala Val Glu Lys Trp Trp Gln Glu Leu Glu Glu Phe Gly Thr Pro
224           370           375           380
226 Ile Asp Asn Val Leu Thr Pro Glu Leu Trp Asp Leu Lys Gly Lys Ala
227 385           390           395           400
229 Ile Gly His Tyr Thr Gln Met Ala Trp Asp Arg Thr Tyr Arg Leu Gly
230           405           410           415
232 Cys Gly Ile Ala Asn Cys Pro Lys Met Ser Tyr Val Val Cys His Tyr
233           420           425           430
235 Gly Pro Ala Gly Asn Arg Lys Asn Asn Lys Ile Tyr Glu Ile Gly Asp
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246 <211> LENGTH: 1422
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248 <213> ORGANISM: Artificial Sequence
250 <220> FEATURE:
251 <223> OTHER INFORMATION: Description of Artificial Sequence:VAP-2 cDNA
252 Nucleotide Sequence
254 <400> SEQUENCE: 4
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257 gacgacaagg ttgtagaagc acttggtggt cttgatgatg aactgctaac cgaacatgtg 180
258 tgtaacaaat caacgatcac tcagctacag caggagatca tcttgacaac ccacaatgaa 240
259 ttacgaagat cattggcttt cggaaagcaa agaaacaaga gaggtctcat gaacggtgcg 300
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261 acctcctgcc ctcagcactt tatgccgcaa tcggtacttg gctccaacgc tcagcttttt 420
262 aagcgtttct atttttattt tgatgggcac gactctactg tacatatgcg aaacgcgatg 480
263 aagtattggt ggcagcaagg tgaagaaaaa ggcaatgagg atcagaaaaa tagattctat 540
264 gccagacgaa attatttttg atgggcaaac atggcaaaag gaaaaacata tcgagttgga 600
265 tgctcgata ttatgtgcgg cgacggtgaa tctgcacttt tcaactgtct ttataacgaa 660
266 aaagcccaat gcgaaaaaga aatgatttac gaaaatggaa aaccctgctg tgaggataaa 720
267 gactgtttca catatccagg atcaaaatgt ttagtacctg aaggattatg tcaagcacct 780

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270 gaatggaatg gagaaacaaa cacttcccag ccaaaggcta gtcaaagatg caaaatggag 960
271 tatgactgca tgttggaaacg gtttgacaaa aactgggcaa ataattgcgt ttttgacacac 1020
272 tcggcacatt acgaaagacc gaatcagggt cagaatctct acatgagttc tttctcaaac 1080
273 cctgataccta gaagccttat acatacggcc gtcgagaagt ggtggcagga attggaggag 1140
274 ttcggtactc caattgataa cgttctgaca cccgaattgt gggatttgaa agggaaagcg 1200
275 ataggacatt acactcagat ggccctggat cgtacttacc gtcttggttg tggaaatcgca 1260
276 aactgtccga agatgtcgta cgtggtttgt cactatgggc cagcaggcaa cagaaagaac 1320
277 aataaaatct atgaaatcgg ggatccttgc gaagtcgatg atgattgccg gattggaaca 1380
278 gattgtgaaa agacaacttc tttatgtgtg atctcaaaat aa 1422

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281 <210> SEQ ID NO: 5

282 <211> LENGTH: 218

283 <212> TYPE: PRT

284 <213> ORGANISM: Artificial Sequence

286 <220> FEATURE:

287 <223> OTHER INFORMATION: Description of Artificial Sequence:Clustal W

288 Alignment of VAP-1, VAP-2, and Selected Other

289 Nematode VA Proteins.

291 <400> SEQUENCE: 5

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296 20 25 30
298 Thr Asp Lys Asp Arg Gln Ala Phe Leu Asp Phe His Asn Asn Ala Arg
299 35 40 45
301 Arg Arg Val Ala Lys Gly Val Glu Asp Ser Asn Ser Gly Lys Leu Asn
302 50 55 60
304 Pro Ala Lys Asn Met Tyr Lys Leu Ser Trp Asp Cys Ala Met Glu Gln
305 65 70 75 80
307 Gln Leu Gln Asp Ala Ile Gln Ser Cys Pro Ser Ala Phe Ala Gly Ile
308 85 90 95
310 Gln Gly Val Ala Gln Asn Val Met Ser Trp Ser Ser Ser Gly Gly Phe
311 100 105 110
313 Pro Asp Pro Ser Val Lys Ile Glu Gln Thr Leu Ser Gly Trp Trp Ser
314 115 120 125
316 Gly Ala Lys Lys Asn Gly Val Gly Pro Asp Asn Lys Tyr Asn Gly Gly
317 130 135 140
319 Gly Leu Phe Ala Phe Ser Asn Met Val Tyr Ser Glu Thr Thr Lys Leu
320 145 150 155 160
322 Gly Cys Ala Tyr Lys Val Cys Gly Thr Lys Leu Ala Val Ser Cys Ile
323 165 170 175
325 Tyr Asn Gly Val Gly Tyr Ile Thr Asn Gln Pro Met Trp Glu Thr Gly
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VERIFICATION SUMMARY

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